

SEQUENCE LISTING

<110> KATZ, RUTH
JIANG, FENG

<120> DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS

<130> UTSC:658US

<140> UNKNOWN

<141> 2001-08-06

<160> 11

<170> PatentIn Ver. 2.1

<210> 1

<211> 722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (18) .. (680)

<400> 1

```

cgctaacgc tgccaac atg gtg ttc agg cgc ttc gtg gag gtt ggc cgg      50
      Met Val Phe Arg Arg Phe Val Glu Val Gly Arg
              1              5              10

gtg gcc tat gtc tcc ttt gga cct cat gcc gga aaa ttg gtc gcg att      98
Val Ala Tyr Val Ser Phe Gly Pro His Ala Gly Lys Leu Val Ala Ile
              15              20              25

gta gat gtt att gat cag aac agg gct ttg gtc gat gga cct tgc act      146
Val Asp Val Ile Asp Gln Asn Arg Ala Leu Val Asp Gly Pro Cys Thr
              30              35              40

caa gtg agg aga cag gcc atg cct ttc aag tgc atg cag ctc act gat      194
Gln Val Arg Arg Gln Ala Met Pro Phe Lys Cys Met Gln Leu Thr Asp
              45              50              55

ttc atc ctc aag ttt ctg cac agt gcc cac cag aag tat gtc cga caa      242
Phe Ile Leu Lys Phe Leu His Ser Ala His Gln Lys Tyr Val Arg Gln
              60              65              70              75

gcc tgg cag aag gca gac atc aat aca aaa tgg gca gcc aca cga tgg      290
Ala Trp Gln Lys Ala Asp Ile Asn Thr Lys Trp Ala Ala Thr Arg Trp
              80              85              90

gcc aag aag att gaa gcc aga gaa agg aaa gcc aag atg aca gat ttt      338
Ala Lys Lys Ile Glu Ala Arg Glu Arg Lys Ala Lys Met Thr Asp Phe
              95              100              105

gat cgt ttt aaa gtt atg aag gca aag aaa atg agg aac aga ata atc      386

```


0992304-030601

130	135	140
Gly Thr Lys Gly Thr Ala	Ala Ala Ala Ala Ala	Ala Ala Ala Ala Ala
145	150	155
Ala Ala Ala Ala Lys Val	Pro Ala Lys Lys Ile Thr	Ala Ala Ser Lys
165	170	175
Lys Ala Pro Ala Gln Lys Val	Pro Ala Gln Lys Ala Thr	Gly Gln Lys
180	185	190
Ala Ala Pro Ala Pro Lys Ala	Gln Lys Gly Gln Lys Ala	Pro Ala Gln
195	200	205
Lys Ala Pro Ala Pro Lys Ala	Ser Gly Lys Lys Ala	
210	215	220

<210> 3
 <211> 2797
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (83) .. (1672)

<400> 3
 acccacgcgt ctggccgcgg gccgcctctg cggcagcgct agtcgccttc tccgaatcgg 60

ctccgcacag ctaggagaaa ag atg ttc act gtg ctg acc cgc caa cca tgt 112
 Met Phe Thr Val Leu Thr Arg Gln Pro Cys
 1 5 10

gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
 15 20 25

ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
 30 35 40

atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
 45 50 55

att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
 60 65 70

tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc 352
 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
 75 80 85 90

aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
 95 100 105

caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448

090304-080601

Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	
110 115 120	
cag gtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc	496
Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	
125 130 135	
acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat	544
Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	
140 145 150	
gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac	592
Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	
155 160 165 170	
ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga	640
Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	
175 180 185	
tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg	688
Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	
190 195 200	
tgg cac atg tgg gtg cac ccg cat gga gtg gaa acc acg ggt gcc ctg	736
Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	
205 210 215	
gac tta ggt ggt gcc tcc acc caa ata tcc ttc gtg gca gga gag aag	784
Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	
220 225 230	
atg gat ctg aac acc agc gac atc atg cag gtg tcc ctg tat ggc tac	832
Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr	
235 240 245 250	
gta tac acg ctc tac aca cac agc ttc cag tgc tat ggc cgg aat gag	880
Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu	
255 260 265	
gct gag aag aag ttt ctg gca atg ctc ctg cag aat tct cct acc aaa	928
Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys	
270 275 280	
aac cat ctc acc aat ccc tgt tac cct cgg gat tat agc atc agc ttc	976
Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe	
285 290 295	
acc atg ggc cat gta ttt gat agc ctg tgc act gtg gac cag agg cca	1024
Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro	
300 305 310	
gaa agt tat aac ccc aat gat gtc atc act ttt gaa gga act ggg gac	1072
Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp	
315 320 325 330	

cca tct ctg tgt aag gag aag gtg gct tcc ata ttt gac ttc aaa gct	1120
Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala	
335 340 345	
tgc cat gat caa gaa acc tgt tct ttt gat ggg gtt tat cag cca aag	1168
Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys	
350 355 360	
att aaa ggg cca ttt gtg gct ttt gca gga ttc tac tac aca gcc agt	1216
Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser	
365 370 375	
gct tta aat ctt tca ggt agc ttt tcc ctg gac acc ttc aac tcc agc	1264
Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser	
380 385 390	
acc tgg aat ttc tgc tca cag aat tgg agt cag ctc cca ctg ctg ctc	1312
Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu Leu	
395 400 405 410	
ccc aaa ttt gat gag gta tat gcc cgc tct tac tgc ttc tca gcc aac	1360
Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn	
415 420 425	
tac atc tac cac ttg ttt gtg aac ggt tac aaa ttc aca gag gag act	1408
Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr	
430 435 440	
tgg ccc caa ata cac ttt gaa aaa gaa gtg ggg aat agc agc ata gcc	1456
Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala	
445 450 455	
tgg tct ctt ggc tac atg ctc agc ctg acc aac cag atc cca gct gaa	1504
Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu	
460 465 470	
agc cct ctg atc cgt ctg ccc ata gaa cca cct gtc ttt gtg ggc acc	1552
Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Pro Val Phe Val Gly Thr	
475 480 485 490	
ctc gct ttc ttc aca gtg gca gcc ttg ctg tgt ctg gca ttt ctt gca	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
tac ctg tgt tca gca acc aga aga aag agg cac tcc gag cat gcc ttt	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
gac cat gca gtg gat tct gac tga gccttcaaag cagctcctgg agtccaatgg	1702
Asp His Ala Val Asp Ser Asp	
525 530	
ctgcttagag tcagcctggg tggcaccagg caatgcaggt gaagtggctg ccttcaggaa	1762
atacaactaa ctaaaatcaa acacctaggt cacgtgcctc tcaaatactg atttctgcca	1822

cagcacctct tgaggcatcc cttggctatt ctgtgcatat tgttcttcag agacctcact 1882
 acccacatgc tgatctattg gggaacagag aagagacagg ccactaaggt caggctcttt 1942
 atattaagtt cccagagga agagtaagtt gagaaggtat cagtttaatg ttgaagaatt 2002
 gacctcaggg ctcagtttcc atttccctcc ctcagtattc ttcctggcaa gataccatt 2062
 aagcatttcg ccaatcagaa tctcatttta tagtttttcc cattgggtctt taactaagac 2122
 tttcttgtag caatctcgta agcagtgaac cccctcagat cagtagaata tagtatctgg 2182
 gggagaagac ttacttcctt cagggcagca gccacagcca ggcttctgtc atacaggtag 2242
 atcccgaagc acagagacat aaaaaaggtc tcccagaaaa ctatagacca ttctccaagt 2302
 ggaattccca cttagggctc tggtcactag attgcaacct gtgtgtttgt catcatctc 2362
 atctcaccat tgtattgcta tgccctccca taaaaacaca ttgatcccta gcaagattat 2422
 tgcattccag attttactgc ctttgctagg cttttgctta gcaaagggt gactttccat 2482
 tgttatcatg gtgtatatat ttttgtcacc attcccacaa gtatacttga tgttgtcata 2542
 gaacgaacat cctactctat gatttactaa ccaattactt tccagatca tagacctctc 2602
 tgcatagtag tcataggtct tgactttggg gaaagaaaaag gaagctgcag gaatatttat 2662
 ctccaaagtc gaatgagaaa gaactccagc aaatccaatg gctacaaact aaaaatcagc 2722
 attatttcat attgctgttt cttagctgaa tatggaataa agaactatta ttttattttg 2782
 aaaaaaaaaa aaaaa 2797

<210> 4
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Phe Thr Val Leu Thr Arg Gln Pro Cys Glu Gln Ala Gly Leu Lys
 1 5 10 15
 Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala Leu Val Val Leu Leu Val
 20 25 30
 Ser Ile Val Val Leu Val Ser Ile Thr Val Ile Gln Ile His Lys Gln
 35 40 45
 Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly Ile Val Leu Asp Ala Gly
 50 55 60
 Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln Trp Pro Ala Glu Lys Glu
 65 70 75 80
 Asn Asn Thr Gly Val Val Ser Gln Thr Phe Lys Cys Ser Val Lys Gly
 85 90 95
 Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro Gln Asp Val Pro Arg Ala

Phe	Glu	Glu	Cys	Met	Gln	Lys	Val	Lys	Gly	Gln	Val	Pro	Ser	His	Leu		
		115					120					125					
His	Gly	Ser	Thr	Pro	Ile	His	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu		
	130					135					140						
Leu	Arg	Leu	Gln	Asn	Glu	Thr	Ala	Ala	Asn	Glu	Val	Leu	Glu	Ser	Ile		
145					150					155					160		
Gln	Ser	Tyr	Phe	Lys	Ser	Gln	Pro	Phe	Asp	Phe	Arg	Gly	Ala	Gln	Ile		
				165					170						175		
Ile	Ser	Gly	Gln	Glu	Glu	Gly	Val	Tyr	Gly	Trp	Ile	Thr	Ala	Asn	Tyr		
			180					185						190			
Leu	Met	Gly	Asn	Phe	Leu	Glu	Lys	Asn	Leu	Trp	His	Met	Trp	Val	His		
		195					200					205					
Pro	His	Gly	Val	Glu	Thr	Thr	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser		
	210					215						220					
Thr	Gln	Ile	Ser	Phe	Val	Ala	Gly	Glu	Lys	Met	Asp	Leu	Asn	Thr	Ser		
225					230					235					240		
Asp	Ile	Met	Gln	Val	Ser	Leu	Tyr	Gly	Tyr	Val	Tyr	Thr	Leu	Tyr	Thr		
				245					250						255		
His	Ser	Phe	Gln	Cys	Tyr	Gly	Arg	Asn	Glu	Ala	Glu	Lys	Lys	Phe	Leu		
			260					265					270				
Ala	Met	Leu	Leu	Gln	Asn	Ser	Pro	Thr	Lys	Asn	His	Leu	Thr	Asn	Pro		
		275					280					285					
Cys	Tyr	Pro	Arg	Asp	Tyr	Ser	Ile	Ser	Phe	Thr	Met	Gly	His	Val	Phe		
	290					295					300						
Asp	Ser	Leu	Cys	Thr	Val	Asp	Gln	Arg	Pro	Glu	Ser	Tyr	Asn	Pro	Asn		
305					310					315					320		
Asp	Val	Ile	Thr	Phe	Glu	Gly	Thr	Gly	Asp	Pro	Ser	Leu	Cys	Lys	Glu		
				325					330						335		
Lys	Val	Ala	Ser	Ile	Phe	Asp	Phe	Lys	Ala	Cys	His	Asp	Gln	Glu	Thr		
			340					345						350			
Cys	Ser	Phe	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Ile	Lys	Gly	Pro	Phe	Val		
		355					360						365				
Ala	Phe	Ala	Gly	Phe	Tyr	Tyr	Thr	Ala	Ser	Ala	Leu	Asn	Leu	Ser	Gly		
	370					375					380						
Ser	Phe	Ser	Leu	Asp	Thr	Phe	Asn	Ser	Ser	Thr	Trp	Asn	Phe	Cys	Ser		
385					390					395					400		
Gln	Asn	Trp	Ser	Gln	Leu	Pro	Leu	Leu	Leu	Pro	Lys	Phe	Asp	Glu	Val		
				405					410						415		
Tyr	Ala	Arg	Ser	Tyr	Cys	Phe	Ser	Ala	Asn	Tyr	Ile	Tyr	His	Leu	Phe		
			420					425					430				

<210> 5
 <211> 3771
 <212> DNA
 <213> Homo sapiens

<220>
 <221> prim_transcript
 <222> (921)..(3751)

<400> 5
 ccatggcccc ttcatagggg ccccaattgt gactttattg ctcattagtct cttccctgcc 60
 ttggtggctc tcatccccc aacctgaatg cagaagtctt ggtcctagac tcaactccgt 120
 gccacccttc agcctacgtt gtgggttcct gctaagctga gcattttacct aacaatcaag 180
 acttctgaca gtccacagtc ctgcccccaa accccttgg atttctcttt ttcaagggtg 240
 tttcggctag gagagtgagc gtggcttggg tgagggcaga tagggtggga gcatggggca 300
 tgtatggatg agaccttgac aaagggaccc cggaggaaag acagggggccc tttccccctt 360
 tgtcctggaa acccggtca gccccagccc ttgcccattc tgctgctgct gcttgggtacc 420
 ttccacaagg ccagactcct ctccacaaag ctgtggtctg caccagctcc tctgggtctc 480
 ctctctgcc tgctgagggc cgctcctag cctggctgcc aatcacagga gaaaggggtt 540
 gggattttgt ttgtgcctct gtctgagcag agaattggctg ataggcactg agcggtgccc 600
 tggagagccc ctctgtccct gctatcccca tctcccctgg ccagacttc tgcccttcac 660
 gcccatccct gaccagcagc cccactcagt ctgggtctct ggtgccagct gtatagacat 720
 gccactgaa cccaggccag agctgggtgat gcgtggggct attttaagca cagcctcttg 780
 gctgcacac tcccctggcc cccagccccc agcagctcag ctactggtca cctgccaccg 840
 cctggaatgc tgattggcag ttggttgggg tgggtggggg ctgggaagac actattataa 900
 agctgggagt gttgggaagc agcgtcccc gtccagagtc ctctgtggtc cctgctgcc 960
 ccatggccac tcaccgcctc gtgatggtcc ggcagggcga gagcacatgg aaccaggaga 1020
 accgtttctg tggctggttc gatgcagagc tgagtgaana ggggaccgag gaggccaagc 1080
 ggggagccaa ggccatcaag gatgccaaag tggagtttga catctgctac acgtcagtgc 1140
 tgaagcgggc catcccagc ctctgggcca tccctggacg caccgaccag atgtgggtgc 1200
 ctgtggtgag cacttgccgc ttcaatgagc ggcattacgg gggcctcaca ggcctcaaca 1260
 aggcaaaaac ggccgccaag cacggggagg agcaggtgaa gatctggagg cgtccttctg 1320
 acatcccgcc gccccgatg gacgagaagc acccctaata caactccatt agcaagggtg 1380
 gctgcctttg ctgggaaggc ctctgggaag ctgcagagtg gggagtcggg tgggggcccc 1440
 ctggcttggg agggaaagca gcgtgcctgt gtccccagc agcgtcggtg cgcaggcctg 1500
 aagcccgggg aactccccac ctgcgagagc ctcaaggaca ccattgcccg ggccctgccc 1560
 ttctggaacg aggagattgt tcccagatc aaggccggca agcagtgct cattgcagcc 1620
 cacgggaaca gcctgcgggg cattgtcaag cacctggaag gtaggccacc ttcaggagcc 1680
 tgggcagggt ggggtggcag cagccagctg gcttctcatc tcagcaaagt ctctcgccat 1740
 gaccagcttt ctagcgtggc tccacatcat tcaactgaaa gaggtgaga agccattttt 1800
 tagttttgtg aaattttccc catttctgtg taactggaca cactccacag gggctgactg 1860
 cactcgaagc tcgtgtgtc ccgaggtggg gcaggctcca aaggtggcat ctgccaaggg 1920
 acaccagctc aggaacagga agggctgggc ttagagcatc tggtccaaa tcccaactta 1980
 ctgtggggcc ctggacaagc cacctccatc tctgggcctc tcccttttcc ggggtgggtg 2040
 ggagctcccc ctggtactga attcctcttg atgtaggctt ggacccctcg cagggccctc 2100
 ccccatcagg tcctcagaat ccctgcagta gcttcaccac ctatctccct ctggagcccc 2160
 tctctgggca aaggaaagac caatcaaaag aggggtgcag gactatggag tggccagact 2220
 ctgggcttgc agctgggctc ccactgaaga gcaagggtc acaaatggg ccgggagtgca 2280
 tgggcgcagt aaggcctcgc ccagagtgc tggcacctcc gtccgcctcc cacttagta 2340
 ttctgacaca agggcagctc aaattagcat ctgaatgacc ttaaagcttg ttgagtcctg 2400
 gaaaggctag aagggtgtgc cccagacctc ctgctcctag ggcgttggg cagttggcca 2460
 gagcaccag accggcaggc cccggagacc cagccagccc caagcctgcc cgctccaaac 2520
 acggacacct ggcacctggc actggggcca ggcagagggg aggaccacct gcctcctctc 2580


```

ccttcgggag acttcatgca gccccatgac cctcccacag cctggtttgg ggaaagggga 2640
cgcaactttt gtggtgaata tgagggattt cactctgact ccccagagaa cattttctta 2700
aaccctccc tgacaggagc aggggtggag tggcgcaaac atcaaaggct gagctgctat 2760
tcccagctca ggggctgcag gaggcaggca gggctcagggt tcgaccaggc tcggcctccc 2820
tgtccctcct ccagctccat tccgcacttg ctctctgtt caggatgtct agaatttaga 2880
gcacttttaga aacaaagggt gctgggcacg gtggctcact cctgtaatcc cagcactttg 2940
ggaggctgag gcaggcagat cacctgaggt caggagtttg agaccagcct gaccaacatg 3000
gtaaaacccg tttctactaa aaatacaaaa ttagccgggt gtggtggcgc tcacctgtaa 3060
tcccagctac ttgggaggct gaggcagaat cacttcaacc caggagatgg aggttgagct 3120
gagccaagat cgtgccactg cactccagcc tgggcaagag gagtaaaact ccactctcaa 3180
aaaaagaaaa agaaaaagaa aagaaaaaaa aaaaccaaag ggtgagtgtc cttcctgac 3240
cctcaacttc agtctggctg gagtcacact gggctgaggg aactatggac agcaccacca 3300
cagatcacag ccacttggtt ggggctgaag tccccatttt ttccaccact gggctatttc 3360
tgtaggctgc ttggtctaac tcagttactc cttgaccttt ggcaacattt ctgtggcctc 3420
gttctcaggg ctgggaagga attggtgcca ggggaactgg ctctgtggac cataaaggct 3480
acatagtgtc tgctgtgtaa acaggctggg gacagagggg ctaaggacac ctattccttc 3540
cggcataggg atgtcagacc aggcgatcat ggagctgaac ctgcccacgg ggatccccat 3600
tgtgtatgag ctgaacaagg agctgaagcc caccaagccc atgcagttcc tgggtgatga 3660
ggaaacggtg cggaaggcca tggaggtgtt ggctgcccag ggcaaggcca agtgaggggt 3720
gggcttgggc aataaaggca cctcccccaa cagcctggag tctccagcgc a 3771

```

<210> 6
 <211> 992
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242)..(583)

<400> 6
 ttttgtgaga gagecgcagc gccgcctctt ctctcgcgcc ctgcctctt cctccgcctc 60
 ctctctcgcc tcttctgccc tcttccccgc ttccgcgcgc gccactccag cctaattcca 120
 accccagggc gaagggtttt ttattttatt ccgttttctc gccactacag cctcctgaca 180
 aggtgatccg ggcgggcccc gcaggaattt tatccctca ccggcctcac actagtatcg 240

c atg tcc act atc cag aac ctc caa tct ttc gac ccc ttt gct gat gca 289
 Met Ser Thr Ile Gln Asn Leu Gln Ser Phe Asp Pro Phe Ala Asp Ala
 1 5 10 15

act aag ggt gac gac tta ctc ccg gca ggg act gag gat tac att cat 337
 Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly Thr Glu Asp Tyr Ile His
 20 25 30

ata aga atc cag caa cgg aac ggc aga aag aca ctg act act gtt cag 385
 Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys Thr Leu Thr Val Gln
 35 40 45

ggc att gca gat gat tat gac aaa aag aaa ctt gtg aaa gct ttc aaa 433
 Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys Leu Val Lys Ala Phe Lys
 50 55 60

<212> DNA
<213> Homo sapiens

<400> 8
caccatgtcc actatccaga acctccaatc tttcgacccc tttgctgatg caactaaggg 60
tgacgactta ctcccgagcag ggactgagga ttacattcat ataagaatcc agcaacggaa 120
cggcagaaaag acactgacta ctgttcaggg cattgcagat gattatgaca aaaagaaact 180
tgtgaaagct ttcaaaaaga aatttgcttg taatgggtact gtgattgaac atcctgaata 240
cggagaggtt attcagcttc aaggtgacca aagaaaaaac atctgccagt ttctcttgga 300
ggttggcatt gtaaaggagg aacagcttaa ggttcattgga ttcaagggcg agcttcgagg 360
tcaccatttc gaaggtgaagc ctatccctaa ccctctcttc ggtctcgatt ctacgcgtac 420
cggtcattcat caccatcacc attga 445

<210> 9
<211> 146
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic Peptide

<400> 9
Met Ser Thr Ile Gln Asn Leu Gln Ser Phe Asp Pro Phe Ala Asp Ala
1 5 10 15
Thr Lys Gly Asp Asp Leu Leu Pro Ala Gly Thr Glu Asp Tyr Ile His
20 25 30
Ile Arg Ile Gln Gln Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln
35 40 45
Gly Ile Ala Asp Asp Tyr Asp Lys Lys Lys Leu Val Lys Ala Phe Lys
50 55 60
Lys Lys Phe Ala Cys Asn Gly Thr Val Ile Glu His Pro Glu Tyr Gly
65 70 75 80
Glu Val Ile Gln Leu Gln Gly Asp Gln Arg Lys Asn Ile Cys Gln Phe
85 90 95
Leu Leu Glu Val Gly Ile Val Lys Glu Glu Gln Leu Lys Val His Gly
100 105 110
Phe Lys Gly Glu Leu Arg Gly His Pro Phe Glu Gly Lys Pro Ile Pro
115 120 125
Asn Pro Leu Leu Gly Leu Asp Ser Thr Arg Thr Gly His His His His
130 135 140
His His
145

090304-40E2660

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 10
caccatgtcc actatccaga acctcc

26

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 11
gaatccatga accttaagct gtcc

24

09923304-030601